VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

On page 7, line 4, please replace with the following paragraphs:

Figure 1 is a schematic of a matrix protein array used to react 96 antibodies (Ab.1-Ab.96) with samples in each compartment of columns I-XII and rows A-H. Compartment A XII contains 16 biological samples of two types for differential analysis with antibody no. 12.

Figure 2 is a schematic of a matrix protein array used to react 96 identifier molecules (Idf.1-Idf.96) in each compartment of columns I-XII and rows A-H. Compartment A XII contains 16 biological samples of 4 types for differential analysis with identifier molecule no. 12.

On page 13, line 25, please replace with the following paragraph:

For example, as represented in Figure 1, the solid support **1** containing the matrix protein arrays may be composed of 96 separate compartments **2**. In this embodiment, each compartment contains the same type, number and composition of biological materials. In this example, 8 samples are derived from normal cells **3a** (represented by white circle in the drawing) and 8 are derived from diseased **4a** samples (represented by dark circles in the drawing). Each biological sample from disease and normal may correspond to total protein extract, processed cell derivatives, tissues or any sample to be interrogated in high throughput fashion. Different identifiers, preferentially antibodies, are used to analyze the matrix protein arrays and to secure data for the differential reactivity of each sample with each antibody.

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On page 14, line 4, please replace with the following paragraph:

Referring to Figure 2, as with the antibodies in the embodiment of Figure 1, the discrete identifier molecules are exposed to each compartment containing biological samples for differential analysis. As noted above, while the number of compartments **2** comprising the matrix protein arrays may vary, a single compartment **2** can be comprised of any combination of biological samples **3**, **4**, **5**, **6**. For example, the protein in the biological samples **3**, **4** are derived from at least two, or more, optimally distinct physiological states. For example, the compartment may contain samples derived from a normal **3** patient, an early stage cancer **4a**, a more progressed vascularized tumor **5**, and a diffuse metastasized malignancy **6**. By reacting a large number of samples with discrete identifier molecules a protein expression profile is created based on the identity of the reaction between the sample and the identifier molecule. Also, the distinct character of the samples may be established in many ways, for example, the sample may contain the same type of the sample tissue from different individuals, the same type of tissue at different developmental stages of the same individual, the same type of tissue in different pathological or physiological conditions, the same cell type exposed to a biological, chemical or physical stimuli during period of time. The matrix may contain the same type of tissue from different species. The matrix protein arrays preferably receive distinct identifiers in each compartment leading to direct information of protein expression profiling for each member of the matrix.

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IN THE CLAIMS:

1. A method to analyze gene expression comprised of:

providing a plurality of samples of biological material comprising an expression product of a gene sequence, arranged in a discrete compartment, wherein the plurality of samples contain gene expression products derived from at least two distinct biological conditions that may exhibit differential gene expression,

contacting each of the plurality of samples with an antibody wherein the antibody is specific to the expression product of a gene sequence, and

correlating the reaction between the antibody and the plurality of samples with expression of the gene sequence.

4. The method of claim 1 wherein the plurality of samples of biological material is comprised of samples from a human disease exhibiting differential gene expression.

7. The method of claim 1 further comprising the step of repeating the contacting step to identify a plurality of gene sequences associated with the [a] biological condition.